Wen Li Lim, Yuhani Yusof, Norhayati Rosli

Futures & Trends Research Group, Faculty Industrial Sciences & Technology, Universiti Malaysia Pahang, Leburaya Tun Razak, 26300 Gambang, Pahang.

DNA SPLICING LANGUAGE PREDICTOR

ABSTRACT:

Recombinant DNA technology, joining two DNA molecules together to produce new genetic combinations is of value to medicine, agriculture and science industry. This new invention of software programming has been developed using Visual Basic in order to predict the number pattern of resulted molecules after the cut and paste phenomenon of two double-stranded DNA, based on the theorems that have been formulated by using Y-G splicing system. Besides, the characteristics of restriction enzymes in terms of palindromic and inverse complement properties are also determined.

INTRODUCTION:

A DNA string is cut by restriction enzyme producing sticky ends fragments.

The sticky ends fragments are then glued together with the existence of ligase, generating new molecules

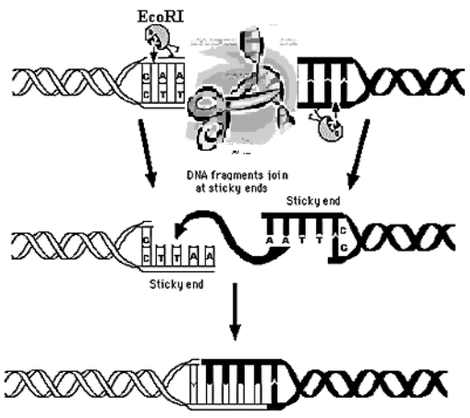


Figure 1: Recombinant of DNA

Helping you to determine the number of new patterns

PRELIMINARIES:

Palindromic [4]

A string *I* of dsDNA is said to be palindromic if the sequence from the left side of the upper single strand is equal with the sequence from the right side of the lower single strand.

Inverse Complement

A string x is an inverse complement to another string y if $x = y'$, where $x, y \in A^*$. Two strings I_1 and I_2 of dsDNA are said to be inverse complement to each other if the sequence from the left side of the upper single strand of I_1 is equal to the complement of first upper single strand with the sequence from the right side in I_2.

RESULTS:

THEOREMS IN THE PROGRAM DEVELOPMENT:

Theorem 1:
In a splicing system that contains one initial string and one non-palindromic crossing site rule, there will be only one pattern of single stage splicing language.

Theorem 2:
An initial string that contains one palindromic crossing site rule produces three patterns of splicing languages.

Corollary 1:
Splicing system that contains two palindromic rules with same crossing sites generates the same number of splicing language as the splicing system that consists of two inverse complement palindromic rules.

Theorem 3:
The number of splicing languages generated from a splicing system that consists of two strings and two non palindromic rules with different crossing sites are the same if the crossing sites of two rules are inverse complement to each other.

Theorem 4:
In a splicing system that contains one initial string of two rules with each palindromic and non palindromic crossing site respectively; there will be three patterns of single stage splicing language.

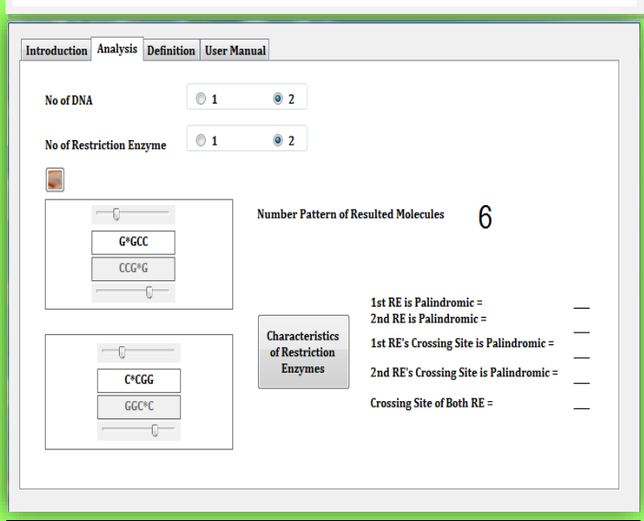
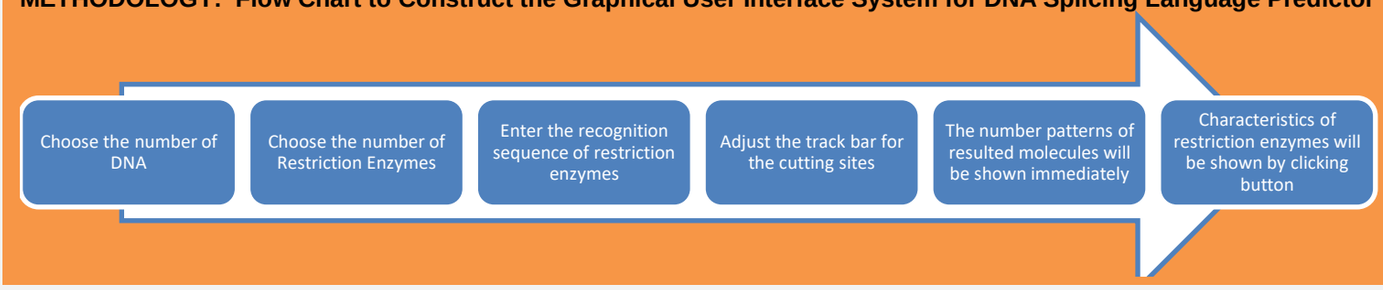


Figure 2: User Friendly Interface of DNA Splicing Language

METHODOLOGY: Flow Chart to Construct the Graphical User Interface System for DNA Splicing Language Predictor



REFERENCES:

1. T.Head, Formal language theory and DNA: an analysis of the generative capacity of specific recombinant behaviors. Bulletin of mathematical biology, 49(6),737-759, 1987
2. R. H. Tamarin, *Principles of Genetic*, 7th. Ed. USA: The Mac-Graw Hill Companies, 2001
3. D. Hartl, *Genetics*, Jones and Bartlett Publishers, Aug 5, 2011
4. Y. Yusof, "DNA Splicing System Inspired by Bio Molecular Operations", Ph.D. Thesis, Universiti Teknologi Malaysia of Malaysia, 2012
5. Research Biolabs Sdn. Bhd. *New England Biolabs2011-12 Catalogue & Technical Reference.* USA: Catalogue. 2011

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